Computational Biologist

VRC, NIAID

The Dale and Betty Bumpers Vaccine Research Center (VRC) at the National Institute of Allergy and Infectious Diseases (NIAID), National Institutes of Health (NIH), is dedicated to improving global human health through the rigorous pursuit of effective vaccines for human diseases, including HIV and emerging infectious disease. The VRC translates the latest concepts in disease pathogenesis and immunology into new vaccine strategies, providing safe and effective means to prevent and control human diseases.

The VRC vaccine development process is inherently interdisciplinary, combining basic, translational, and applied research in immunology, virology, disease pathogenesis, molecular biology, structural biology, and clinical investigation, along with regulatory science and clinical material manufacture, to move novel technologies from the laboratory into the clinic in a safe and compliant manner. These areas complement each other and promote collaboration and exchange, both within the center and with outside collaborators, providing an effective foundation for vaccine development.

We are seeking a computational structural biologist interested in protein design. Candidates should have experience with a broad range of computational tools associated with protein structure and protein-protein interactions and have an interest in applying these tools to an exciting series of problems associated with vaccine design. The successful applicant will join a computational biology team that is integrated with VRC scientists working on the development of an effective HIV-1 vaccine. This team currently consists of several staff mentoring two postdoctoral fellows.

Re-eliciting a target antibody that recognizes a specific scaffold is a major goal of vaccine design. Current efforts at the VRC with computational transplanted antibody epitopes (to create epitope-scaffold immunogens) appear to provide a solution to the re-elicitation problem. Other efforts with surface modification have permitted the "antigenic-cloaking" of the HIV-1 env, so that only the target epitope remains.

The success of these efforts has led to the creation of a new onsite computational biology team, which will be expected to continue current collaborations and to enhance current HIV-1 vaccine design efforts. These efforts involve 1) crystallographic definition of a site of vulnerability on the HIV-1 env to antibody-mediated neutralization, 2) design of immunogens based on the vulnerable site, and 3) design of select binding ligands to decipher the elicited response. In addition to assisting with structure-based HIV-1 vaccine efforts, successful applicants will be encouraged to pursue independently other avenues of computational vaccine-design efforts for other viral diseases, including Ebola, Marburg, and influenza viruses. Interactions with graduate students and postdoctoral fellows related to protein production and computational design will also be encouraged.

See more about the computational biology team at www.niaid.nih.gov/labsandresources/labs/aboutlabs/vrc/structuralbioinform.

Salary will be based on the individual's qualifications and experience, in the range of $80,000 – $100,000. This position is subject to a background investigation.

Specific Requirements
- Ph.D. in biophysics or related field with experience in computational biology and with protein design
- Excellent oral and written communication skills

Application Information
- Submit a current curriculum vitae and three letters of reference.

Contact
To apply or for more information, contact National Institute of Allergy and Infectious Diseases, Vaccine Research Center, c/o Vaccine Research Center Administrative Support Branch, Attn: Mrs. Renita Farrington, Building 40, Room 1118, 40 Convent Drive, Bethesda, MD 20892–3013 or brookr@mail.nih.gov.

Deadline
Applications are due by close of business **July 31, 2011**.

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